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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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(without alignments)
59.222 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

61.5 267 22 AAB90827 61.5 537 22 AAM41777	62.8 429 20 AAY25520 62.8 491 22 ABG28562 62.8 693 22 ABG28564	1 49 62.8 262 20 AAY25521 E. coli 2 49 62.8 262 22 AAU34559 E. coli 3 49 62.8 262 22 AAE02203 Escheri 4 49 62.8 269 22 AAU38231 Salmone.	No. Score Match Length DB ID Descript.
	E. coli Fabl prote Novel human diagno Novel human diagno	E. coli mutant Fab E. coli cellular p Escherichia coli N Salmonella typhi c.	Description

ALIGNMENTS

×	PR	PR	×	ΡF	×	PD	×	PN	×	FT	FΤ	Ϋ́	FH	×	SO	SO	×	ΚW	ΚW	ΚW	ΚW	ΚW	×	Z X	DŢ	XX	AC	XX	ID	RESULT 1 AAY25521
	23-JAN-1998;	26-JAN-1998;		22-JAN-1999;		29-JUL-1999.		W09937800-A1.				Protein	Key		Synthetic.	Escherichia coli.		resistance; NSA	detergent; mout	antiprotozoal;	fatty acid bios	Fabl; enoyl ACI		F COlimitant Eabl protoin	30-SEP-1999 (1		AAY25521;		AAY25521 standa	5521 .
	98US-0072244.	98US-0013440.		99WO-US01288.						/note≖ "No stop codon given in specification"	/label= Fab1	1262	Location/Qualifiers			li.		resistance; NSAM; non-specific antimicrobial; mutant.	thwash; toothpaste; contraceptive; inhibitor; triclosan;	antiprotozoal; antiparasitic; antiviral; soap; infection; disinfectant;	fatty acid biosynthesis; detection; antibacterial; antifungal; treatment;	Fabl; enoyl ACP reductase; acyl carrier protein; antimicrobial; therapy;	ייייי לייייייייייייייייייייייייייייייי	5571 510+0-5	(first entry)				AAY25521 standard; Protein; 262 AA.	

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       AAU34559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fungal, yeast and protozoal infections, in both humans and animals, and (ii) in disinfectants, detergents, soaps, mouthwashes, toothpaste's and also contraceptive devices. The invention describes methods for (1) identifying a (I) from its effect on enzymatic activity of ER, (2) identifying a (I) from its ability to inhibit fatty acid biosynthesis in a microbe, (3) identifying a (I) that interacts with a mutant ER, (4) identifying (I) that inhibit proliferation or viability of a microbe that is resistant to triclosan or to NSAM (non-specific antimicrobials). This sequence repersents a mutant Escherichia coli Fabl protein which interacts with the enoyl-acyl carrier protein (ACP) reductase to illustrate the method of the invention.
                                                                                21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contacting ER with test compound and detecting any interaction. The identified antimicrobials have antibacterial, antifungal, antiprotozoal, antiparasitic and antiviral activity. The products of the invention are used (1) therapeutically to treat a wide variety of viral, bacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 77; Fig 2; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TUFT ) TUFTS COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for identifying antimicrobials
(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                        WO200170955-A2
                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                            E. coli cellular proliferation protein #140
                                                                                                                                                                                                                                                                                                                                                                                         AAU34559;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAU34559 standard; Protein; 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying antimicrobials that target enoyl acyl carrier protein reductase, for therapeutic use and for incorporation into e.g. soaps
                                                    27-NOV-2000;
22-DEC-2000;
                                                                                                                                                            21-MAR-2001;
                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                                                                                  antibiotic; antibacterial;
                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular
                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (I) that interact with an enoyl acyl carrier protein (ACP) reduct(ER) polypeptide, which is essential for fatty acid biosynthesis,
                                     16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 VRYMANAMGPEGVRV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AA;
                                    2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                                                                              2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                    drug design.
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                  proliferation
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2.2;
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PROSESSES OF TRANSPORT OF TRANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FabI; high throughput method; fatty acid biosynthesis; therapy;
bacterial enzyme; biological agent screening; otitis media; empyema;
bacterial tracheitis; acute epiglottitis; thyroiditis; lung abscess;
infective endocarditis; secretory diarrhoea; splenic; retroperitoneal;
intrarenal; perincphric; cerebral; cutaneous; abscess; blepharitis;
conjunctivitis; keratitis; endophthalmitis; preseptal; orbital;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
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                                                                                                                                                                                                                                                                                                                                                               septic arthritis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                           cellulitis; darcryocystitis; epididymitis; abscess; toxic shock syndrome; impetigo; folliculitis; wound infection; bacterial myositis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE02203 standard; Protein; 262 AA.
                                                                                                                                                                                                                                                                                                                             acyl carrier protein
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                                                                                                                                03-MAY-2001.
                                                                                                                                                                                                   WO200130988-A1
                                                                                                                                                                                                                                                                 Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coli NADPH-dependent enoyl-ACP reductase (FabI).
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Xu HH;
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Pred. No. 2
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27-OCT-1999;

26-OCT-2000; 2000WO-US29451.

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                                                                                                                                                                                                                                                                                                                                                                                                   respiratory tract (e.g. offitis media, bacterial tracheltis, acute epiglottitis, thyroiditis), lower respiratory (e.g. empyema, lung abscess), cardiac (e.g. infective endocarditis), gastrointestinal (e.g. secretory diarrhoea, splenic abscess, retroperitoneal abscess), central nervous system (e.g. cerebral abscess), eye (e.g. blepharitis, central conjunctivitis, keratitis, endophthalmitis, perseptal and orbital cellulitis, darcryocystitis), kidney and urinary tract (e.g. splenic abscess), central cepididynitis, intrarenal and perinephric abscess, toxic shock syndrome), skin (e.g. impetigo, folliculitis, cutaneous abscess, cellulitis, wound infection, bacterial myositis) and bone and joint (e.g. septic arthitis, osteomyelitis).

The present sequence is Escherichia coli NADPH-dependent enoyl-ACP (acyl carrier protein) reductase (Fabl). In fatty acid blosynthetic pathway, dehydration by Fabs leads to trans-2-enoyl-ACP
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
 21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK)
                                                        21-MAR-2001; 2001WO-US09180
                                                                                                     WO200170955-A2
                                                                                                                         Salmonella typhi
                                                                                                                                              Antisense; prokaryotic cellular antibiotic; antibacterial; drug
                                                                                                                                                                             Salmonella typhi cellular proliferation protein #122.
                                                                                                                                                                                                      14-FEB-2002
                                                                                                                                                                                                                              AAU38231;
                                                                                                                                                                                                                                                AAU38231 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        which is in turn converted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for screening biological agents affecting fatty acid biosynthesis. Agonists and antagonists of fab (fatty acid biosynthesis) are used to inhibit, prevent or treat diseases such as infections of the upper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a high throughput method for biological agents affecting fatty acid biosynthesis, comprises contacting a bacterial enzymatic pathway with enzymes. The met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 15; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High throughput method for screening for biological agents against fatty acid biosynthesis comprises contacting a bacterial enzymatic pathway with enzymes e.g. malonyl-CoA:ACP transacylase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dewolf W,
                                                                                                                                                                                                                                                                                                          170 VRYMANAMGPEGVRV 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention
                                                                                                                                                                                                                                                                                                                               MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-316332/33.
                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kallender H,
                                                                                                                                                                                                                                                                                                                                                                                                  262
 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lonsdale
                                                                                                                                                                                                                                                                                                                                                                                                                       to acyl-ACP by FabI.
                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 2
Pred. No. 2.2;
4; Mismatches
                                                                                                                                                        proliferation protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT;
                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                           Length 262
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for screening
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                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                          RESULT 5
AAY25520
В
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                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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•
                                                      Protein
                                                                                      Escherichia
                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                                                                                                         AAY25520
                                                                                                                                                                                                                                               AAY25520 standard;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R, Yamamoto RT,
                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               269
                                                                                      coli
                                                                                                                                                                                                                                                                                                                                                                                               AA;
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invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form with introduction.
/note= "in-frame stop codon encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                 /note- "No start or stop codon given in specification" Misc-difference 74\,
                                                                                                                                                                                                                                                                                                                Fabl; enoyl ACP reductase; acyl carrier protein; antimicrobial; therapy; fatty acid biosynthesis; detection; antibacterial; antifungal; treatment antiprotozoal; antiparasitic; antiviral; soap; infection; disinfectant; detergent; mouthwash; toothpaste; contraceptive; inhibitor; triclosan; resistance; NSAM; non-specific antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       itp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-2000; 2000US-253625P
22-DEC-2000; 2000US-257931P
16-FEB-2001; 2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli Fabl protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRYMANAMGPEGVRV 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Xu HH;
                                                                                                                                                                          Location/Qualifiers
1..429
                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                      treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 6
ABG28562
CC (I) that interact with an encyl acyl carrier protein (ACP) reductase CC (ER) polypeptide, which is essential for fatty acid biosynthesis, by CC contacting ER with test compound and detecting any interaction. The CC identified antimicrobials have antibacterial, antifungal, antiprotozoal, CC used (i) therapeutically to treat a wide variety of viral, bacterial, CC fungal, yeast and protozoal infections, in both humans and animals, and CC (ii) in disinfectants, detergents, soaps, mouthwashes, toothpaste's and CC (also contraceptive devices. The invention describes methods for (1) CC also contraceptive devices. The invention describes methods for (2) CC identifying a (I) from its effect on enzymatic activity of ER, (2) CC identifying a (I) from its ability to inhibit fatty acid biosynthesis in CC identifying (I) that inhibit proliferation or viability of a microbe that CC is resistant to triclosan or to NSAM (non-specific antimicrobials). This CC sequence represents the Escherichia coli Fabl protein which interacts CC with the enoyl-acyl carrier protein (ACP) reductase to illustrate the
                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09937800-AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-1998;
23-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 68-70; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and detergents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying antimicrobials that target enoyl acyl carrier protein reductase, for therapeutic use and for incorporation into e.g. soaps {\sf reductase}, for therapeutic use and for incorporation into e.g. soaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX88347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for identifying antimicrobials
               Homo sapiens.
                                                Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                   ABG28562 standard; Protein; 491
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                    18-FEB-2002
                                                                                                                                                                   ABG28562;
                                                                                                                                                                                                                                                                                    300 VRYMANAMGPEGVRV 314
                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                   1 MRYRASALGSDGVRV 15
                                                                                              human diagnostic protein #28553.
                                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMurry LM;
                                                                                                                                                                                                                                                                                                                                                                                                                     429 AA;
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                  (first entry)
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98US-0072244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "in-frame stop codon encoded 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "in-frame stop codon encoded by TAA"
398
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                                                                                                                                                                                                                                                                                                                                                                     62.8%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 2
Pred. No. 3.7;
4; Mismatches
                                                                                                                                                                                                     AA
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                                                                   forensic;
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DR
XX
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess responsible for genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and nolvneptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification, but was obtained in electroniat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide (II) sequences. (I) is useful as myoridisation probes, polypeptide chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                    ABG28564 standard; Protein; 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic amino acid sequences of the invention.
                                                          Homo sapiens
                                                                                                                                                          Novel human diagnostic protein #28555.
                                                                                                                                                                                                  18-FEB-2002
                                                                                                                                                                                                                                            ABG28564;
                                                                                              food supplement; medical
                                                                                                                                                                                                                                                                                                                                                                                      378 VRYMANAMGPEGVRV 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRYRASALGSDGVRV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polymorlactides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques (I), (II) is useful in gene therapy techniques (I), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as conditional control of the supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating conditional control of the polypeptide and polypucleotide sequences have applications in the polypeptide and polypucleotide sequences have applications in conditions for genetic disorders or other traits to assess biodiversity conditions and to produce other types of data and products dependent on DNA and conditions conditions of the invention.

Condition acid sequences. ABG00010-ABG30377 represent novel human conditions of the invention.

Condition of the sequence data for this patent did not appear in the printed construction, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 9
            12-APR-2001
                                                                               Homo sapiens.
                                                                                                                 arteriosclerosis
                                                                                                                          Human; shear stress-response protein; vascular disease;
                                                                                                                                                               Human shear stress-response protein SEQ ID NO: 171.
                                                                                                                                                                                                      15-JUN-2001
                                                                                                                                                                                                                                                                    AAB90827 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                           601 VRYMANAMGPEGVRV 615
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 58923; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                693 AA;
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                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 2
Pred. No. 6.2;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 693;
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RESULT 9
AAM41777
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Best Local
                                                         03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                          21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
 Tang YT,
                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                        (HYSE-) HYSEQ INC
                                                                                                                                                    26-DEC-2000;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                 WO200153312-A1
                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 6708.
                                                                                                                                                                                                                                                                                                                                                                             AAM41777;
                                                                                                                                                                                                                                                                                                                                                                                               AAM41777 standard; Protein; 537 AA.
                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 35; Page 664-665; 678pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequences, proteins encoded by them and antibodies against them useful in diagnosis and treatment of vascular disease caused by arteriosclerosis -
                                                                                                                                                                                                                                                leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nojima H,
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(NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ALGSDGVRVT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Liu C,
                                                        2000US-0488725
2000US-0552317
2000US-0598042
2000US-0620312
2000US-0623450
2000US-0662191
2000US-0662191
2000US-0693036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                    2000WO-US34263
                                              2000US-0727344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
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Asundi V,

Chen R,

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Qian XB,

Ren F,

Wang

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RESULT 10
ABG10171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzahelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activiny chamatetic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
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Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #10162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG10171 standard; Protein; 1050 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification.
                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                       N-PSDB; AAS74358.
                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                        WPI; 2001-639362/73.
                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ALGSDGVRVT 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 AA;
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Goodrich F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 48; 100.0%; Pred. No.
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7;
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Best Local S
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 40530; 103pp; English.
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide (II) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM39991 standard; Protein; 1063 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 3136.
                                                                                                                               14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                     03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 ALGSDGVRVT 21
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1050 AA;
                                                                                                                                                                                              2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                     2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 48; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1050;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 10
   25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

16-APR-1999
                                                                                                                   25-FEB-2000;
                                                                                                                                      06-SEP-2000
                                                                                                                                                         EP1033405-A2
                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                Arabidopsis thallana protein fragment SEQ ID NO: 17197.
                                                                                                                                                                                                                                                                                         AAG16520 standard; Protein; 357 AA.
                                                                                                                                                                                                                                                   17-0CT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                       specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442253/47.
N-PSDB; AAI59147.
                                                                                                                                                                                                                                                                                                                                         26 ALGSDGVRVT 35
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                            7 ALGSDGVRVT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; SEQ ID NO 3136; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                   1063 AA;
                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 48; DB ilarity 100.0%; Pred. No. 14; Conservative 0; Mismatches
                                                                                                                   2000EP-0301439
   990S-0121825
990S-0123180
990S-0125748
990S-0125788
990S-0126785
990S-0126785
990S-0127462
990S-0128234
990S-0128234
990S-0128714
990S-0128714
990S-0128714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
14;
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, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                               Length 1063;
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Zhang J;
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22-JUN 1999
23-JUN 1999
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24-JUN 1999
28-JUN 1999
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01-JUL 1999
01-JUL 1999
01-JUL 1999
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09-JUL-1999;
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21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
28-MAY-1999
01-JUN-1999
01-JUN-1999
04-JUN-1999
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10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
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16-JUN-1999;
17-JUN-1999;
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21-JUN-1999;
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19-MAY-1999
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23-APR-1999;
      990S-0134768
990S-0134941
990S-0135124
990S-0135323
990S-0136021
990S-0136021
990S-0137528
990S-0137528
990S-0138034
990S-0138034
990S-0139453
990S-0140853
990S-0140823
990S-0140823
990S-0142803
990S-0144085
990S-0144085
990S-0144085
990S-0144333
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99US-0134218.
99US-0134219.
99US-0134221.
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99US-0132407.
99US-0132484.
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99US-0130510.
99US-0130891.
99US-0131449.
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99US-0132863
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RESULT 13
AAU36258
ID AAU362
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT 1999
21-OCT 1999
21-OCT 1999
21-OCT 1999
22-OCT 1999
22-OCT 1999
25-OCT 1999
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14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
                                                                                                                21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa cellular proliferation protein #248
                                                                                                                                                                                                                                                                                                                      AAU36258;
                                   WPI; 2001-611495/70.
N-PSDB; AAS54117.
                                                                                                                                                                                                                                                        antibiotic;
                                                                                                                                                                                                                                                         Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                     14-FEB-2002
                                                                                                                                                                                                                                                                                                                                        AAU36258
      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                 21-MAR-2001;
                                                                                                                                                                                                  27-SEP-2001
                                                                                                                                                                                                                      WO200170955-A2
                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
                                                                      Haselbeck
                                                                                        (ELIT-)
                                                              Yamamoto
                                                                                                           16-FEB
                                                                                                                                                                                                                                                                                                                                                                                    43 RASALGNTGLKVT
                                                                                                                                                                                                                                                                                                                                                                                              4 RASALGSDGVRVT
                                                                                                            -2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 69.2
9; Conservative
                                                                                        ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                        standard; Protein; 265 AA.
                                                              RT,
                                                                                                          ; 2000US-191078P.
; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                 2001WO-US09180
                                                              Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0159331

99US-0159638

99US-0159584

99US-0160767

99US-0160768

99US-0160768

99US-0160814

99US-0160815

99US-0160815

99US-0160981

99US-0160981

99US-0161406

99US-0161406

99US-0161359

99US-0161359

99US-0161359

99US-0161359

99US-0161392

99US-0161392

99US-0161920

99US-0161920

99US-0161920

99US-0161920

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99US-0161920
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                                                                                                                                                                                                                                                                                                                                                                                                                                 57.7%;
69.2%;
                                                                       KL,
                                                                       Zyskind
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB Pred. No. 15;
                                                                        JW,
                                                                         Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                         D,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 357;
                                                                         Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
             of.
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                                                                          Carr GJ;
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99US-0144352
99US-0144844
99US-0144864
99US-0145086
99US-0145086
99US-0145089
99US-0145089
99US-0145089
99US-0145214
99US-0145218
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99US-0151086
99US-0151089
99US-

18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;

10-SEP-1999;

13 SEP-1999
16 SEP-1999
16 SEP-1999
20 SEP-1999
22 SEP-1999
23 SEP-1999
24 SEP-1999
24 SEP-1999
06 OCT-1999
06 OCT-1999
07 OCT-1999
17 OCT-1999
11 OCT-1999

20-JUL-1999 20-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 27-JUL-1999 28-JUL-1999 29-AUG-1999 29-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 21-AUG-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antiblotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC invention is also useful for the identification of potential new targets of or antiblotic development. The antisense nucleic acids can also be used CC and to obtain antibodies capable of binding to the express these proteins, CC programmes. The antisense nucleic acids can also be used CC and to obtain antibodies capable of binding to the expressed proteins, CC programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
A method has been developed for: (1) inhibiting growth of a bacterium; (11) alleviating the symptoms of a bacterial infection in a subject; (111) inhibiting activity of enoyl reductase enzyme in a cell; or (iv) altering a pathway of fatty acid synthesis in a bacterium, comprises contacting the bacterium, subject or cell with a novel compound (I) or
                                                                                                                                                       Inhibiting growth of bacteria gemfibrozil or related compoun
                                                                                                                                                                                                                N-PSDB; AAX19775
                                                                                                                                                                                                                               WPI; 1997-448377/41.
                                                                                                                                                                                                                                                                    Della-Latta P,
                                                                                                                                                                                                                                                                                                  (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                          29-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                            28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L. pneumophila FabI enoyl reductase homologue protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legionella pneumophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Legionella pneumophila; FabI; enoyl reductase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99839 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 VRYLAGSLGAEGTRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Seq ID No 11851; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRYRASALGSDGVRV 15
                                                                                                                 2; Fig 21B; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth inhibition; bacterium; infection
                                                                                                                                                                                                                                                                                                                                          96US-0608712.
                                                                                                                                                                                                                                                                  Kabbash C,
                                                                                                                                                                                                                                                                                                                                                                          97WO-US03158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.4%;
53.3%;
                                                                                                                                                       compound
                                                                                                                                                                                                                                                          Shuman HA, Silverstein SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
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Pred. No.
                                                                                                                                                                   _ by contacting the bacteria with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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ABB93255

ID ABB9

XX ABB9

AC ABB8

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                   Matches
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                                                                                                                                                                                                      suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding the greater useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                          (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using
                                                                                                                                      Sequence
                                                                                                                                                                                                useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 2466; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tietjen K, Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200210210-A2
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Search completed: January 16, 2003, 10:12:11 Job time : 38 secs

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Result
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Perfect score:
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SP_Barchea:*

Sp_barchea:*

Sp_barchea:*

Sp_barceria

Sp_fungi:*

Sp_invert

Sp_nmamna'

Sp_mamna'

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Sp_phar

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Gapop 10.0 , Gapext 0.5
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sp_virus:*
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16 ORZ7C7
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Ogerb6 mus musculu
Ogerp73 pasteurella
O827c7 salmonella
O51891 proteus mir
O89972 ralstonia s
O8wq34 leishmania
O9re03 legionella
O9f1k5 burkholderi
O91pk0 arabidopsis
O915f6 salmonella
O935m8 salmonella
O935m8 salmonella
O92mq0 rhizobium m
O81792 arabidopsis
O9m068 arabidopsis
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Q8UHC5 Q9FJ82 Q97Q18	064874 Q8T692 Q92PP8	Q9Z5F4 Q9Z5F4 Q8X5I9 Q9ZSV3	P73172 Q9P9W1	Q48571 Q94BN8 Q9FLO1	Q8S1Q8 Q8RR23 Q59485	Q92D51 Q8Y8D5 Q8YQD6	Q9L8E7 Q9K151 Q9JSS8	Q9S1S8 Q9F2K4 Q96PW2 Q9KYZ2 Q9KYZ2
Q8uhc5 agrobacter1 Q9fj82 arabidopsis Q9fq18 streptococc	9	Q99ys retsimanta Q925f4 myxococcus Q8x519 escherichia Q92sv3 rhizobium m			oryza sati streptomyce lactobacill		Q9l8e7 vibrio harv Q9k151 neisseria m Q9jss8 neisseria m	

ALIGNMENTS

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1 MRYRASALGSDGVRVT 16	Query Match 100.0%; Score 78; DB 11; Length 1044; Best Local Similarity 100.0%; Pred. No. 0.00014; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	\$M00015; IQ; 2. \$M00242; MYSC; 1. E 1044 AA; 119876 MW;	Pfam; PF00063; MyOSIn_head; 1. PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; 1.	InterPro; IPROUVO49; IQ_FEGION. InterPro; IPROUBLO9; myosin_head. Dfam. DEDDG13, TO. 3			"A Myosin I Isoform in the Nucleus."; Science 0:0-0(2000).	<pre>Ke Y., Settlage R.E., Shabanowitz J., Hunt D.F., Hozak P., de Lanerolle P.;</pre>	stic-Dragovich L., Stojiljkovic L.,	SEQUENCE FROM N.A.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	Mus musculus (Mouse).	MYO1C.	U1-JUN-2002 (TrEMBLrel. 21, Last annotation update)	(Trembliel.		Q9ERB6 PRELIMINARY; PRT; 1044 AA.	OULT 1

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1 MRYRASALGSDGVRVT 16

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RESULT
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01-JUN-2001
01-JUN-2002
                           "Complete genome sequence of a multiple drug resistant enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
EMBL; AL627270; CAD01621.1; -
InterPro; IPR002198; ADH_short.
                                                                                                             MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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  Complete proteome
                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                             Salmonella typhi.
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                    Pfam; PF00106; adh_short; 1.
                                                                                                   Whitehead
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 RFMAAALGKDGIRV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SDR) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conserv
                                                                                                 S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.1%;
64.3%;
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17,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922E5EBE8B0C8963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                               subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260
                                                                                                                                                                                                                                                                                                                                                                                                           262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
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                                                                                       Salmonella
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RESULT 5
Q8Y07
ID 08Y0
AC 08Y0
AC 08Y0
DT 01-M
DT 01-M
DT 01-M
DT 01-M
CO 0840
CO RALS
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q51891 PRELIMINARY; PRT; Q51891; Q1991; Q1996 (TrEMBLrel. 01, Created 01-NOV-1996 (TrEMBLrel. 01, Last as 01-JUN-2002 (TrEMBLrel. 21, Last as Similar to E.coli EnvM (Fragment).
                                                                                                                                                                    OBYO72 PRELIMINARY; PRT; 264 AA.

QBYO72:
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable enoyl-[acyl-carrier-protein] reductase (EC FABI OR RSC1172 OR RSO4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mirabilis, a prototype of a new class of enzymes.", Eur. J. Biochem. 211:421-425(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U38482;
HSSP; P29132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "MOLECULAR cloning and overexpression of a glutathione transferase
gene from Proteus mirabilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mignogna G., Allocati N., Aceto A., Barra D., Martini F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae
  STRAIN=GMI1000;
                         SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=305;
                                                                                                  Ralstonia
                                                                                                                         Bacteria; Proteobacteria; beta
                                                                                                                                               Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96358500; PubMed=8761466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The amino acid sequence of glutathione transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE=93170270; PubMed=8436105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 VRYMANAMGPEGVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRYRASALGSDGVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                             VRYMANAMGPEGIRV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em. J. 318:157-162(1996).
U38482; AAC44361.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conser
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                                                                                                                                                  solanacearum (Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 AA; 10395 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aceto A.,
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Last annotation update)
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Pred. No. 2.6;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2E442ABB04AFA031 CRC64;
                                                                                                                         monas solanacearum).
subdivision; Ralsto
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                                                                                                                           Ralstonia group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                    1.3.1.9).
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RESULT 7
Q9RE03
ID Q9RE
AC Q9RE
DT 01-M
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DT 01-C
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Best Local s
Matches
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Best Local
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O9REO3; PREL:
O9REO3;
O1-MAY-2000 (TrEI
O1-MAY-2000 (TrEI
O1-DEC-2001 (TrEI
Encyl reductase.
FABI.
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Q8WQ34;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation p265.17, unknown
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A physical map of the Leishmania major Genome Res. 8:135-145(1998).
EMBL; AL359716; CAD19425:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robben J., Grymonprez
Ivens A.C., Quail M.,
Submitted (DEC-2001) t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa;
NCBI_TaxID-5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21681879;
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9; Conser
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 AA;
                                                          (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13,
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                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49507 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.7%;
56.2%;
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64.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B., Weltjens I., Aert R., Volckaert Rajandream M.A., Barrell B.G.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bagherzadeh A., Zhang
                                                 Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 5;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 444;
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Q9LPK0;
01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004866; Carbb_Hex.
InterPro; IPR001540; GH_20.
Pfam; PF03173; CHB_HEX; I.
Pfam; PF007788; Glyco_hydro_20; 1.
PRINTS; PR00738; GLHYDRLASE20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tanaka H., Toyoda H.;

"DNA sequence of chitinase gene cloned from Burkhorderia Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB053088; BAB20043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kabbash C.A., Albala A., Latta P.D., Fei
Silverstein S.C., Shuman H.A.;
"Antibiotic activity of gemfibrozil for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.tuberculosis."
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Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
Legionellaceae; Legionella.
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9; Conserv
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8; Conser
                                                                                                                                                                                                                                                                                                                                                      826 AA;
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  (TrEMBLrel.
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                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                     Score 43;
Pred. No.
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                                                                      PRT;
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19;
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RESULT 10
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Q935M8
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Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Chi J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                Q935M8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20280091; PubMed=10773089; Sherburne C.K., LawLey T.D., Gilmour M.W., Blattner F.R., Burland V., Grotbeck E., Rose D.J., Taylor D.E.; "The complete DNA sequence and analysis of R27, a large IncHI plasmid from Salmonella typhi that is temperature sensitive for transfer."; Nucleic Acids Res. 28:2177-2186(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
01-MAR-2002
                       01-DEC-2001
01-DEC-2001
                                                                        Q935M8;
                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Plasmid. SEQUENCE 151 AA; 18075 MW;
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                       (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21396507; PubMed-11481430;
Capela D. Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Capela D., Backer A., Boutry M., Ccadieu E., Dreano S., Gloux Boistard P., Becker A., Boutry M., Ccadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q92MQ0 PRELIMINARY; PRT; 252 AA. Q92MQ0. Q1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence up 01-MAR-2002 (TrEMBLrel. 20, Last annotation Putative oxidoreductase protein (EC 1.1.1.).
                                                                                                                                                                                                                                                                              Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; ALS91791; CAC47142.1; -.
InterPro; IPR002198; ADH_short.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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EMBL; AL513383; CAD09726.1; -.
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A Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
A Gurjal M., Hong A., Hulzar L., Hyman R.W., Kahn D., Kahn M.L.,
A Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
A Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti psynA megaplasmid.";
A Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
BR EMBL; AE007211; AAK64838.1; -.
CR Feam; PF00106; ADH_short.
CR PROSITE; PS00061; ADH_short; UNKNOWN_1.

PROSITE; PS00061; ADH_Short; UNKNOWN_1.

KW Plasmid; Hypothetical protein; Complete proteome.
KW Plasmid; Hypothetical protein; Complete proteome.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                              EU Arabidopsis sequencing project;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; ALO31135; CAA20030.1; -
Interpro; IPR000719; Euk_pklnase.
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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Submitted (JUL-1998) to
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Rhizobium meliloti (Sinorhizobium meliloti)
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                                                                                                                                                                                                                                 S., Entian K.-D., Hoheisel
Mewes H.W., Mayer K.F.X.,
) to the EMBL/GenBank/DDBJ
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STY_pkinase.
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ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYKG; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KINASE; Serine/threenine-protein kinase.

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PRINTS; PR00109; TYRKINASE.

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SMART; SM00221; STYK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.

PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
-!- SIMILARTY: BELONGS TO THE SER/THR FAMILY
EMBL; AL161587; CAB80276.1; -
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Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase SEQUENCE 415 AA; 45879 MW; 2FAFD025A219F528 CRC64;
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InterPro; IPR007290; Ser_thr_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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SLPO_BACBR
PSA_METJA
FABI_BACSU
GS39_BACSU
VGLM_MCMYK
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Q9hr92 halobacteri
Q48319 halobacteri
P42850 pyrococcus
Q9v2h7 pyrococcus
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Q57830 pyrococcus
P0933 bacillus br
Q57962 methanococc
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P42734 arabidopsis
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2 22	23967; PubMed=1364817;
F A	uer G., Turnow
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RΡ	SEQUENCE FROM N.A.
7 Z	2 / W3110;
RA S	395;
감	"The use of a hybrid genetic system to study the functional
RT ?	synthetase complexes.":
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<u>ල</u> ද	STRAIN=K12 / MC1655.
RX	MEDLINE~97426617; PubMed~9278503:
RA	Bloch C.A., Perna N.T
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먑	"The complete genome sequence of Escherichia coli K-12 ".
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RC	STRAIN=K12;
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RA	i H., Kashimoto K., Kimura S. Kitakawa M
RA	K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura
RA:	Oshima T., S
RA	Yamamoto V Horinghi m
R	"A 570-kb DNA sequence of the Escherichia coli K-12 genome
R 2	Corresponding to the 28.0-40.1 min region on the linkage map.";
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7.7	SECUENCE FROM N.A.

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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frutiger S., Hughes G.J., Pa
Submitted (FEB-1996) to the
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Baldock C., Rafferty J.B., Sedelnikova S.E., Baker P.J., Stuitje A.R.,
Slabas A.R., Hawkes T.R., Rice D.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparing the predicted and observed properties of in the genome of Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                             WEDLINE=99425142; PubMed=10493822;
Ward W.H., Holdgate G.A., Rowsell S., McLean E.G., Pauptit R.A., Clayton E., Nichols W.W., Colls J.G., Minshull C.A., Jude D.A.,
                       MEDLINE=99215552; PubMed=10201369;
Levy C.W., Roujeinikova A., Sedelnikova S.,
Slabas A.R., Rice D.W., Rafferty J.B.;
                                                                                                                                                    MEDLINE-99329134; PubMed=10398587; Stewart M.J., Parikh S., Xiao G., "Structural basis and mechanism of
                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
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                                                                                                                                                                                                                                                 (acyl carrier protein) reductase by triclosan.";
Biochemistry 38:12514-12525(1999).
"Molecular basis of triclosan activity.";
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                                                                                                                                                                                                                                                                                      Kinetic and structural characteristics of the inhibition of enoyl
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                                                                                  -RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                   Mol. Biol. 290:859-865(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robison K., Church G.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND CHARACTERIZATION
                                                                                                                                                          and mechanism of enoyl reductase inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasquali C.,
he SWISS-PROT
                                                                                                                                                                              Tonge P.J., Kisker C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hochstrasser D.F.; data bank.
                                                  Baker P.J., Stuitje A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Inner membrane-associated.
-!- MISCELLANEOUS: THE ANTIBICTIC DIAZABORINE INTERFERES WITH THE ACTIVITY BY BINDING TO THE PROTEIN.
-!- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90766; BAA14841.1; -. EMBL; D90767; BAA14849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M97219; AAA17755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                      FABI_SALTY P16657;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-2DPAGE; P29132; (EcoGene; EG11528; fabI
                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-dependent enoyl-ACP reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                   FABI OR ENVM OR STM1700.
                                                                                                                                                                                                                                                                                                  01-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane;
MEDLINE=90078098; PubMed=2687243;
                     STRAIN-AG701
                                              SEQUENCE FROM N.A
                                                                                                                 Salmonella
                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                               Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 VRYMANAMGPEGVRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRYRASALGSDGVRV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A47681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE005378; AAG56524.1; -. AP002556; BAB35284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE000227; AAC74370.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pri00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-98.
28-JAN-98.
21-SEP-99.
21-JUL-99.
28-OCT-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 AA;
                                                                                                                                                                                                                                                                          (Rel. 15, Created)
(Rel. 33, Last seq
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92
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                                                                                                                                                                                                                                                                                                                                                STANDARD;
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92
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                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                          gamma subdivision;
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Pred. No. 0.
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S->F: PRODUCES TEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434B019F34855956 CRC64;
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                                                                                                                                                                                                                                                                                                                                                        261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                        AΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEMPERATURE - SENSITIVE
                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                 L_BUCAI
                                                                                                                                                                                   P57353;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Enoyl-[acyl-carrier-protein] reductase [NADH]
dependent enoyl-ACP reductase).
FABI OR BUZE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGEN
STRAIN-TOKYO 1998;
MEDLINE-20445173;
                                                                                                                                symbiotic bacterium).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            StyGene; SG10095; fabl.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B43729; B43729.
HSSP; P29132; 1DFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M31806; AAA27059.1; -. EMBL; AE008775; AAL20618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2] Bacteriol.
                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                       FABI_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; NAD; Fatty acid blosynthesis; Antibiotic
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                                                                                                    NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 VRYMANAMGPEGVRV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envM
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MISCELLANEOUS: THE ANTIBIOTIC DIAZABORINE INTERFERES WITH THE ACTIVITY BY BINDING TO THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Acyl-(acyl-carrier protein] + NAD(+) 2,3-dehydroacyl-(acyl-carrier protein] + NADH. PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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f Salmonella typhimurium and Escherichia coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
  PubMed=10993077;
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92
27629
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60.0%;
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G->S: DIAZABORINE RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 1
Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                       260 AA
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+ NADH.
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                                                                                                                                   Buchnera
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                                                                                                                                                                                                                                                                 1.3.1.9) (NADH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., Layman D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Latreille P.,
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Nature 407:81-86(2000).
-i- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + 2,3-dehydroacyl-[acyl-carrier protein] + NADH.
-i- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSY
-i- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
                                                                                                          Cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-i- CATALYTIC ACTIVITY: Acy1-{acy1-carrier protein} + NAD(+)
2,3-dehydroacy1-{acy1-carrier protein} + NADH.
-i- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESI
-i- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-93308081; PubMed-8391534;

Wei T.-F., Ramasubramanian T.S., Pu F., Golden J.W.;

"Anabaena sp. strain PCC 7120 bifA gene encoding a sequence-specif:
DNA-binding protein cloned by in vivo transcriptional interference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Enoyl [acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q05069;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sas
Watanabe A., Iriguchi M., Ishikawa A., Kawashima
Kishida Y., Kohara M., Matsumoto M., Matsuno A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dependent enoyl-ACP reductase). FABI OR ALL4391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NAD; NP_BIND 10 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP001118; BAB12975.1; -. HSSP; P29132; 1DFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                            This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol.
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                                                                                DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175:4025-4035(1993).
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the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28779 MW;
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53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
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м.,
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                                                                                                                                                                                                                                                                                                                                                            Muraki A.,
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                                                                                                                                                                                             NAD(+) -
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                               collaboration
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                     "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).

-i- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = 2,3-dehydroacyl-[acyl-carrier protein] + NADH.

-i- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.

-i- SUBCELLULAR LOCATION: Inner membrane-associated (By similar i- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Encyl-[Acyl-carrier-protein] reductase [NADH]
dependent encyl-ACP reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentine B., Victorio E., Kowalik D.J., Lagrou M. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoang T.T., Schweizer H.P.; "Characterization of Eseudomonas aeruginosa enoyl-acyl carrier reductase (Fabl): a target for the antimicrobial triclosan and role in acylated homoserine lactone synthesis."; J. Bacteriol. 181:5489-5497(1999).
                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 15692 / PAO1;
MEDLINE=99395061; PubMed=10464225;
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Pfam; PF00106; adh_short; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10984043;
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258,
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Yuan Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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requires a license agreement (See http://www.isb-sib.ch/announce/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R
Sulston J., Thierry Mieg J., Thomas K., Vaudhan K.,
Partners D., Parson M., Partners M., Vaughan K.,
Partners D., Partners M., Partners M., Vaughan K.,
Partners D., Partners M., Partners M., Vaughan K.,
Partners D., Partners M., Partners M., Vaughan K.,
Partners M., 
                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases -i- ALTERNATIVE PRODUCTS: 2 isoforms; a and b (shown he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAEEL
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EMBL; AE004607; AAG05195.1;
HSSP; P29132; IDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston
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Pfam; PF00106; adh_short;
                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                       entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: 2 isoforms; a produced by alternative splicing. SIMILARITY: TO YEAST RGR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRYLAGSLGAEGTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRYRASALGSDGVRV 15
                                                              229115;
219153;
                                                                                                                                                                                                                                                                                                                                                                                                       S.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002198; ADH_short
                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                         ; CAA82365.1;
; CAA82365.1;
; CAA79550.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE SPLICING
                                                                                                                                                       license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28006 MW;
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53.3%;
                                                                 JOINED.
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omosome III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last annotation update)
Glucan 1,4-alpha-maltoterrahydrolase precursor (EC 3.2.1.60) (G4-
amylase) (Maltotetraose-forming amylase) (Exo-maltotetraohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEST
                                                                                         STRAINEMULL:
MEDLINE-20027472; PubMed-10556241;
Hasegawa K., Kubota M., Matsuura Y.;
"Roles of catalytic residues in alpha-amylases
"Roles of catalytic residues in alpha-amylases
                                                                                                                                                                                                 Yoshloka Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.;
"Crystal structures of a mutant maltotetraose-forming exo-amylase cocrystallized with maltopentaose.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z19153; CAA82366.1; J
EMBL; Z19153; CAA79551.1; -
EMBL; Z29115; CAA79551.1; J
PIR; S28289; S28289
WormPep; C38C10.5; CE20550.
                                   01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1040 IRFRASQMNGDGVNAT 1055
                                                                               amylase."
                                                                                                                                                    STRAIN-MO-19
                                                                                                                                                                                                                                             MEDLINE-97428332; PubMed-9281429;
                                                                                                                                                                                                                                                             STRAIN-MO-19
                                                                                                                                                                                                                                                                                                                "Crystal structure of a maltotetraose-forming Pseudomonas stutzer1.";
                                                                                                                                                                                                                                                                                                                                                      Morishita Y.,
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97271999; PubMed-9126844;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-MO-1
                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND
                                                                                                                                                                                                                                                                                                                                                                                                                         maltotetraose-forming amylase from J. Bacteriol. 171:1333-1339(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujita M., Torigoe
Tsujisaka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89155431; PubMed-2646279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-MO-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMT4_PSEST
P13507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Alternative splicing.

VARSPLIC 671 676 MISSING (IN ISOFORM A)
                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Maltotetraose-forming exo-amylase).
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                                                                                                                                                                                                                                                                                                   Mol. Biol. 267:661-672(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  loning and nucleotide sequence of the gene (amyP) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRYRASALGSDGVRVT 16
in amylaceous polysaccharides so as to remove maltotetraose residues from the non-reducing COFACTOR: BINDS TWO CALCIUM IONS. PATHWAY: Starch degradation.
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                                                                                                                                                                                         271:619-628(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K., Nakada T., Tsusaki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      Matsuura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                       from Pseudomonas stutzeri MO-19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                              VARIANTS
                                                                                                                                                                                                                                                                        VARIANT GLN-240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                           exo-amylase from
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د
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                                                                                          as evidenced by the a maltotetraose-forming
                          chain
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                                                    linkages
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                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                 FAI2_RHIME STANDARD; PRT; 268 AA. P58381; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Enoyl-[acyl-carrier-protein] reductase [NADH] dependent enoyl-ACP reductase 2).
FABI2 OR R00246 OR SMC00326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB;
                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria: alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
   NCBI_TaxID=382;
                      Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNOWN AS THE ALPHA-AMYLASE FAMILY.
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1JDC;
1JDD;
                                                                                                                                                                                                                                                                                            LRQAASALGGAGVKV 130
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Pro: IPR002044: CBD_4.
PF00128; alpha-amylase; 1.
PF00686; CBM_20; 1.
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                                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conser
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15-OCT-97.
15-OCT-97.
15-OCT-97.
15-OCT-97.
24-NOV-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       548 AA;
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                      Sinorhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59876 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          REF.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB Pred. No. 16;
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                                   Rhizobiaceae group;
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P52855; O24414;
O1-OCT-1996 (Rel. 3
O1-OCT-1996 (Rel. 3
30-MAY-2000 (Rel. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S.,
                                                                                                STRAIN=CV. B73; TISSUE=Ear;
STRAIN=CV. B73; TISSUE=Ear;
MEDLINE=97422884; PubMed=9276949;
Bailey-Serres J., Vangala S., Szick K., Le
Bailey-Serres J., Vangala S. Szick K., Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21396507; PubMed=11481430;
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"Acidic phosphoprotein complex of the 60S ribosomal suseedling roots. Components and changes in response to plant Physiol. 114:1293-1305(1997).
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                                                                                                                                                                                                                                                 Submitted (NOV-1995) to
                                                                                                                                                                                                                                                                              STRAIN=cv. W22;
Hamilton D.A., Turcich M.P.,
                                                                                                                                                                                                                                                                                                                                                                            Panicoideae; Andropogoneae; NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Panicoideae; Andropogoneae; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60S acidic RPP1A.
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34, Last sequence update,
39, Last annotation update,
wmal protein P1 (L12).
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                                                                                                Lee C.H.;
OS ribosomal subunit of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable adenylyisulfate kinase (EC 2.7.1.25) (APS kinase)
5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3
                                                                                                                                                                                                                                                                                                                                   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U40147; AAA91168.1; -. EMBL; U62752; AAB71079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                            Nature 390:364-370(1997).
-!- FUNCTION: CATALYZES THE SYNTHESIS OF
-!- CATALYTIC ACTIVITY: ATP + adenylylsul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphotransferase).
CYSC OR AF0288.
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                                                                                                                                            reducing archaeon Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaeoglobaceae; Archaeoglobus.
              -!- SIMILARITY: BELONGS TO THE APS
                                                                                                                                                                 "The complete genome sequence
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SUBUNIT (BY SIMILARITY).
I- PTM: PHOSPHORYLATED.
I- PTM: THE N-TERMINUS IS BLO
I- SIMILARITY: BELONGS TO TH
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                                             PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. INVOLVED IN THE ENERGY-GENERATING SULFUR OXIDATION PATHWAYS OF MANY
                                 CHEMOAUTOTROPHIC MICROBES.
                                                                              phosphoadenyly1sulfate.
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TO THE L12P FAMILY OF RIBOSOMAL PROTEINS
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Pred. No.
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                                                                                                  adenylylsulfate
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               KINASE
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
InterPro; IPR003009; FMN_enzyme.
InterPro; IPR0030052; Triophos_ismrse.
InterPro; IPR000652; Triophos_ismrse; 1.
                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodail strain7.";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JCM 10545 / 7;

MEDLINB-21456156; PubMed-11572479;

MEDLINB-21456156; PubMed-11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Kawarabayasi Y., Hino Y., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
                                                        EMBL; AP000988; BAB67127.1; -
                                                                                                                                                                                                                                                                                                                                                                                 AOKi K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
TPIA OR ST2030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Crenarchaeota; Thermoprote1; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96YZ9;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPIS_SULTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002350; APS_kinase; 1.
TIGRFAMS; TIGR00455; apsk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01583; APS_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001085; AAB90945.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 MGYRVELLDGDGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRYRASALGSDGVR 14
                                                                                                                                                                                                                          PATHWAY: Plays an important role in several metabolic pathways. SUBUNIT: Homotetramer (By similarity). SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                          phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002891; APS_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.7%;
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83
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4535298F48931881 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 AA.
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                                                                    Query Match
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                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAI1_RHIME P58380;
                                                                                                        SEQUENCE
                                                                                                                           Complete proteome. NP_BIND 14
                                                                                                                                                     Oxidoreductase; NAD; Fatty acid biosynthesis; Inner membrane
                                                                                                                                                                               Pfam;
                                                                                                                                                                                                             EMBL; AL591785; CAC45470.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-!- CATALYTIC ACTIVITY: ACYL-!-carrier protein] + NADH.
2,3-dehydroacyl-!acyl-carrier protein] + NADH.
-!- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Botstard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the Chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Enoyl-lacyl-carrier-protein] reductase [NADH] 1 (EC 1.3.1.9) (NADH-dependent enoyl-ACP reductase 1).
EABII OR R00898 OR SMC00005.
                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21396507; PubMed=11481430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGRO0419; tim; 1.

PROSITE; PS00171; TIM; FALSE_NEG.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
Pentose shunt; Complete proteome.

ACT_SITE 93 93 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 YKAIELGADGIGV 200
1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Inner membrane-associated (By similarity). SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                    DEHYDROGENASES/REDUCTASES (SDR) FAMILY
                                                                                                                                                                     PF00106; adh_short;
                                   Similarity
8; Conser
                                                                                                                                                                                      IPR002198; ADH_short.
                                                                                                        272 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 AA; 24898 MW;
                                 Conservative
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                                                                                                      29148 MW;
                                                  48.7%;
                                                                                                                       40
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                                                Score 38;
Pred. No.
                                                                                                                 NAD (BY SIMILARITY)
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                                 Mismatches
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                                                               DB 1; Length 272;
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                                                                                                                                                                                                      RESULT 14
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Best Local
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15-JUN-2002 (Rel. 41, Last annotation update)
Glutamate-1-semialdehyde 2,1-aminomutase (EC
                       P11092;
01-JUL-1989 (
01-JUL-1989 (
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20150912; PubMed=10688204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00713; hemL; 1.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000954; Aminotran_3.
InterPro; IPR004639; HemL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P24630; 2GSA.
Protein cyaE precursor.
                                                                                                                                              CYAE_BORPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphyrin biosynthesis; Isomerase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                         241 YRASYLGSYGI
                                                                                                                                                                                                                                                                                                                                                 3 YRASALGSDGV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathway: Porphyrin biosynthesis by the C5 pathway; second step. SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate = 5-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aminolevulinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00202; aminotran_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL139076; CAB73118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11168;
                                   (Rel. 11, Created)
(Rel. 11, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: Cytoplasmic (Potential)
BELONGS TO CLASS-III OF PYRIDOXAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40,
                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46092 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       48.7%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRIDOXAL PHOSPHATE (BY SIMILARITY).; 7811526A5AEDA57D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
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Glaser P., Sakamoto H., Bellalou J., Ullmann A., Danchin A.;
"Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-
naemolysin bifunctional protein of Bordetella pertussis.";
EMBO J. 7:3997-4004(1988).
1- FUNCTION: CYAE IS NECESSARY FOR TRANSPORT OF CALMODULIN-SENSITIVE
ADENYLATE CYCLASE-HEWOLYSIN (CYCLOLYSIN).
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murpby L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Parker S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                            Q10510;

Q1-QCT-1996 (Rel. 34, Created)

Q1-QCT-1996 (Rel. 34, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Hypothetical protein Rv2226.

RV2226 QR MT2285 QR MTCY427.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
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Hemolysis; Transport; Outer membrane; Signal
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                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                    STRAIN=H37Rv;
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                                                                                                                                                                                                 MEDLINE-98295987; PubMed-9634230;
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63.6%;
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; 29A4F21D377FC957 CRC64;
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RC STRAIN-CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DoBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA ROLonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Bishal W.;
RM Bishal W.;
RT Index genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
RT Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration collaboration on the European Bioinformatics Institute. There are no restrictions on its between the Swiss Institute of Bioinformatics and the EMBL outstation on one of the European Bioinformatics Institute. There are no restrictions on its composite this statement is not removed. Usage by and for commercial comparison of the EMBL, 270692; CAA94649.1: -.
CR EMBL; 270692; CAA94649.1: -.
DR EMBL; 270692; CAA94649.1: -.
DR TIGR, MT2285; -.
DR TIGR, MT2
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                    is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/laa/backfiles1.pep:*
                    US-08-804 227C-4
US-08-637-759B-480
US-08-871-355A-480
US-09-201-945-480
US-09-292-412-2
US-09-420-786A-3
US-09-347-803-10
US-09-199-637A-47
US-09-199-637A-47
US-09-199-637A-6
US-09-347-903-126
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US-09-041-991A-6
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PCT-US96-03916-6
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Sequence 5, Appli
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ALIGNMENTS	US-09-041-991A-8	US-09-275-925-7	US-09-073-594-7	US-08-653-740-7	US-09-042-709A-20	US-09-542-403-2	US-08-957-302A-2	US-08-529-654-4	US-09-199-637A-349	US-09-721-689-4	US-09-721-832-4	US-09-722-139-4	US-09-603-567-2	US-09-262-749-2	US-09-022-669-2	US-08-795-927-4	US-08-980-357-23	US-08-286-819A-23
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Query Match
Best Local Similarity
Watches 9; Conserve
                                                                                     TOPOLOGY: US-08-241-766-8
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US-08-241-766-8
                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATAINE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARRE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,766
FILLING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08241766 Patent No. 5686590
                                                                                                                                                                                      TELEFAX: (415) 494-07:
TELEX: 706141
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 25237-20003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JACOBS, W. R.
APPLICANT: BANBRJEE, A.
APPLICANT: BANBRJEE, A.
APPLICANT: delisle, G. W.
APPLICANT: WILSON, T. M.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING
NUMBER OF SEQUENCES: 14
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                       TELEPHONE: (415) ...
TELEPHONE: (415) 494-0792
                                                                                                                      STRANDEDNESS:
                                                                                                                                         TYPE:
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CITY: Palo Alto
STATE: CA
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STREET: 755 Page Mill Road
                                                                                                                                                       LENGTH:
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                Conservative
                                62.8%;
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            Score 49; DB 1;
Pred. No. 0.51;
4; Mismatches
                                             Length 262;
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                                                                                                                                                                                                Sequence 12, Application US/09347803
Patent No. 6274379
                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAN: (415) 494-0792
TELEX: 706141
CURRENT APPLICATION NUMBER: US/09/347,803
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,952
EARLIER FILING DATE: July 15, 1998
                                                                       APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Orozco, Buddy
TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
FILE REFERENCE: BB-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: BANERJEE, A.
APPLICANT: WILSON, T. M.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inha AGENT
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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170 VRYMANAMGPEGVRV 184
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NAME: MONROY, GLADYS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Телетах: (--
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                   170 VRYMANAMGPEGVRV 184
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Pred. No. 0.51;
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Query Match
Best Local Similarity
Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Oryza sativa 
US-09-347-803-12
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PCT-US96-03916-6
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RESULT 5
                                                                                                                                                                           PCT-US96-03916-6
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SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Applicati
GENERAL INFORMATION:
                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                         TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

ADDROLUM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wild, Martha A.

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 03
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 ASALGDDGV 128
                                               921 YECTVLISDGTRVT 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ASALGSDGV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                               3 YRASALGSDGVRVT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
Y: U.S.A.
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                                                                                                                                                                                                                          amino acid
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                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cooper & Dunham LLP
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                                                                                                                               48.7%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/126,597
                                                                                                                                                                                                                                                                                                                                                        28,678
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Pred. No.
                                                                                                                Score 38; DB 5; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                           39116-A
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; Sequence 66, Application PC/TUS9603916 ; GENERAL INFORMATION:

PCT-US96-03916-66

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; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US96-03916-66
                                                                                                                                          APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 3039
FENOTE: 1907-08-14
SEQ ID NO 3039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 5/...
Conservative
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      Matches
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APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                    LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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      Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YRASALGSDGVRVT 16
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1185 Avenue of the Americas
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(212) 391-0525
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      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.7%;
                  47.48;
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; Score 37; DB; Pred. No. 71; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 5;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                      DB 4;
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                                    Length 309;
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              GENERAL INFORMATION:
APPLICANT: Moller, Soren
APPLICANT: Johansen, Charlotte
APPLICANT: Schafer, Thomas
APPLICANT: Schafer, Thomas
APPLICANT: Hoeck, Lisbeth Hedegaard
TITLE OF INVENTION: A 2,6,-b-D-Fructan Hydrolase Enzyme And
TITLE OF INVENTION: Process For Using The Enzyme
FILE REFERENCE: 5540.200-US
CURRENT APPLICATION NUMBER: US/09/397,885
CURRENT FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-041-991A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.4%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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EARLIER APPLICATION NUMBER: PA 1998 01173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sanders, Jay M.
REGISTACTION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375.8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 13-MAR-199
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Sanders, Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Toxins Active Against Pests NUMBER OF SEQUENCES: 10\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                539 RVSSIGSSTIRVT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 RYEHTALGTDPVKL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                        4 RASALGSDGVRVT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Narva Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: PA 1998 01623
EARLIER FILING DATE: 1998-12-08
EARLIER FILING DATE: 1998-09-24
EARLIER FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: 60//11,675
EARLIER APPLICATION NUMBER: 60//11,675
EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis US-09-134-001C-4009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-134-001C-4009
                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-173-508-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.4%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EURCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EURCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: OUR DERNIE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILLING DATE: 1997-11-08
PRIOR FILLING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08173508 Patent No. 5616485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                              APPLICANT: Bartfeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Hadary, David
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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270 LRFRANGQGTDG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 VKYLALDLGEDNIRV 189
STREET: 3000 K Street, CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 7; Conserv
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                                                     ADDRESSEE:
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                            E: Foley & Lardner
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Pred. No. 2.4e+02;
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; MOLECULE TYPE: protein US-08-173-508-2
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Best Local Similarity
"hes 8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300 TELEFAX: 202 672 5399
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
APPLICATE: 24-JUN-1/2.
FILING DATE: 24-JUN-1/2.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,508
APPLICATION NUMBER: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
                                                                                                                                                   COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DOS PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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TELEFAX: 904136
                                                                                                                  SOFTWARE: PatentIn Rel
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REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                    APPLICATION NUMBER: US/08/265,310
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Garven, Shelia
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                                                                                                                                     PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                       Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/173,508
23-DEC-1993
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Pred. No. 1.9e+02;
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US-08-951-742-2
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                           TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                        REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 900176
              MOLECULE TYPE:
                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,742
FILING DATE: 16-CCT-1997
ATTORNEY/ARENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE CONFER NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Z...
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTEN TYPE: Floppy disk
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TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN
TITLE OF INVENTION: BACTERIAL HOST CELLS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.M., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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APPLICANT:
APPLICANT:
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TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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TELEFAX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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REFERENCE/DOCKET NUMBER: 18
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Lawrence T. Malek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phyllis Krygsman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eva Walczyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gisela Soostmeyer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           David Jenish
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            protein
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APPLICANT: LEDEBOER, ADRIANUS M.; MAAT, JAN; VERRIPS, CORNELIS
TITLE OF INVENTION: REGULATORY SEQUENCES OF ALCOHOL OXIDASE; (MOX) AND DIHYDROXYACETONESYNTHASE (DAS) OF HANSENULA POLYMORPHA
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
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                                                                                                                                                                            RESULT 14
5240838-15
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                                                                                                                                                           ;Patent No. 5240838
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US-09-041-991A-4
                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION UMBER: US/09/041
EILING DATE: 13-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: M9,355
REFERENCE/DOCKET NUMBER: MA-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
APPLICATION NUMBER: US/07/587,555 FILING DATE: 24-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins A(
NUMBER OF SEQUENCES: 10
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2421 N.W. 41st Street, Suite A-1
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53.8%;
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50.0%;
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                              Score 36; De Pred. No. 2.
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                .3e+02
                                                                                                                                                                                                                                                                                                                                             Length 635;
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                                                                                                                                                                                                                                                                                                              0,;
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                                                                                                                                                                                                                                                                                                              0;
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APPLICATION NUMBER: 300,211
; FILING DATE: 23-JAN-1989
; APPLICATION NUMBER: 759,315
; FILING DATE: 26-JUL-1985
; SEQ ID NO.15:
; LENGTH: 702
5240838-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Sotteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
APPLICANT: Sutton, Kimberly L.
ITILE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-804-227C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
Search completed: January 16, 2003, 10:13:48 Job time : 15 secs
                                                                             В
                                                                                                                QУ
                                                                                                                                                                                                                               US-08-804-227C-4
                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCIDOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08804227C Patent No. 5876991
                                                                                                                                                        Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                         Query Match
                                                                             1778 RSRAFAAGADGV 1789
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3729 amino acids
                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 NALGEDGVR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: LILLY CORPO
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 SALGSDGVR 14 : | | | | | | |
                                                                                              2 RYRASALGSDGV 13
                                                                                                                                                          Conservative
                                                                                                                                                                           46.28;
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 6; Length 702; Pred. No. 2.6e+02;
                                                                                                                                                      Score 36; DB 2; Length 3729; Pred. No. 1.6e+03; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
            January 16, 2003, 10:13:13; Search time 11 Seconds (without alignments) 28.914 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120991 seqs, 19878514 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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78
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: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyright
                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.3 (c) 1993 - 2003 Compus
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	6	c	۔	w	N	ب.	Result
<u>ა</u>	35	35	35	36	36	36	36	37	37	37	37	37	37	38	38	44	49	49	Score
44.9	44.9	44.9	44.9	46.2	46.2	46.2	46.2	47.4	47.4	47.4	47.4	47.4	47.4	48.7	48.7	56.4	62.8		Query Match
316	256	256	256	1160	358	295	50	1386	1344	1316	943	722	441	1233	315	265	269	262	Length
10	10	10	10	9	9	10	10	9	9	9	10	9	9	9	10	10	10	10	DB
US-09-815-242-13929	US-09-815-242-12892	us-09-815-242-12535	US-09-815-242-5228	US-10-028-072-234	US-09-738-626-4829	US-09-815-242-11279	US-09-864-761-40694	US-10-120-544A-6	US-10-120-544A-20	US-10-120-544A-4	US-09-969-362-5	US-09-738-626-5453	US-09-738-626-4275	US-09-738-626-4312	US-09-815-242-13289	US-09-815-242-11851	US-09-815-242-13824	US-09-815-242-10152	ID
Sequence 13929, A	Sequence 12892, A	Sequence 12535, A	Sequence 5228, Ap	Sequence 234, App	Sequence 4829, Ap	Sequence 11279, A	Sequence 40694, A	Sequence 6, Appli	Sequence 20, Appl	Sequence 4, Appli	Sequence 5, Appli	Sequence 5453, Ap	Sequence 4275, Ap	Sequence 4312, Ap	Sequence 13289, A	Sequence 11851, A	Sequence 13824, A	Sequence 10152, A	Description

Query Match Best Local Similarity

62.8%; 60.0%;

Score 49; DB 10; Pred. No. 0.17;

Length 262;

5	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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42.3	42.3	42.3	42.3	42.3	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	44.2	44.2	44.2	44.2	44.2	44.9	44.9
292	278	278	220	87	11877	11877	3739	3739	1430	911	810	513	423	345	319	319	229	220	3034	3034	677	666	94	558	350
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US-09-738-626-5836	US-10-034-623-26	US-10-027-806-26	US-09-815-242-10428	US-09-864-761-34943	US-09-861-289-6	US-09-860-846-6	US-09-861-289-33	US-09-860-846-33	US-09-740-274-6	US-09-745-763-140	US-09-712-363-281	US-09-833-745-46	US-09-911-317-4	US-09-925-300-1188	US-10-003-014-4	US-10-001-426-4	US-09-965-529-22	US-09-815-242-13735	US-09-737-149-30	US-09-737-149-25	US-09-815-242-10663	US-09-815-242-4933	US-09-976-059-29	US-09-770-517C-2	US-09-765-272-126
Sequence 5836, Ap	Sequence 26, Appl	Sequence 26, Appl	Sequence 10428, A	Sequence 34943, A	Sequence 6, Appli	Sequence 6, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 6, Appli	Sequence 140, App	Sequence 281, App	Sequence 46, Appl	Sequence 4, Appli	Sequence 1188, Ap	Sequence 4, Appl1	Sequence 4, Appli	Sequence 22, Appl	Sequence 13735, A	Sequence 30, Appl	Sequence 25, Appl	Sequence 10663, A	Sequence 4933, Ap	Sequence 29, Appl	Sequence 2, Appli	Sequence 126, App

ALIGNMENTS

RESULT 1

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; TYPE: PRT; ORGANISM: Escherichia coli US-09-815-242-10152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-815-242-10152
: Sequence 10152, Application US/09815242
: Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10152
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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Yamamoto, Robert T.
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall, Daniel
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Query Match
Best Local Similarity
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US-09-815-242-13824
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                                                                                                                                                                                                                                                                                                         US-09-815-242-11851
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Patent No. US20020061569Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13824
                                                                                                                                                                                                                                              GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
            TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                    APPLICANT:
                                                                                                                                                             APPLICANT: APPLICANT:
                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CURRENT APPLICATION NUMBER: US/09/815,242
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177 VRYMANAMGPEGVRV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 VRYMANAMGPEGVRV 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269
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                                                                                                                                                             Zyskind, Judith W. Wall, Daniel
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Zyskind, Judith W.
                                                                          Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                  Carr, Grant J.
                                                                                                                                          Trawick, John D.
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Yamamoto, Robert T.
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Pred. No. 0.18;
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13289
LENGTH: 315
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Best Local :
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
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APPLICANT:
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                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                           ORGANISM: Streptococcus pneumoniae
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                   NAME/KEY: VARIANT
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LOCATION: (1)...(315)
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 4312
LENGTH: 1233
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US-09-738-626-4312
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APPLICANT: IKEDA, MASALU
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
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APPLICANT:
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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Local Similarity 46.7%;
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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OZAKI, AKIO
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OCHIAI, KEIKO
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SENOH, AKIHIRO
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Pred. No. 20;
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Best Local Similarity
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US-09-969-362-5
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                                                            GENERAL INFORMATION:
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Best Local
        APPLICANT: Moller, Soren APPLICANT: Johansen, Charle APPLICANT: Schafer, Thomas
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OCHIAI, KEIKO
YOKOI, HARUHIKO
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57.18;
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58.3%;
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; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTMARE: PatentIn ver. 3.0
; SEQ ID NO 5453
; TENGTH: 722
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
SEQ ID NO 4275
LENGTH: 441
; Sequence 5, Application US/09969362
; Patent No. US20020076790A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-738-626-5453; Sequence 5453, Application US/09738626; Publication No. US20020197605A1
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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Pred. No.
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44;
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RESULT 10
US-10-120-544A-20
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, TYPE: PRT
, ORGANISM: Bacillus popilliae
US-10-120-544A-4
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 09/397,885
PRIOR FILING DATE: 1999-09-17
PRIOR PPLICATION NUMBER: PA 1998 01623
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: 60/101,615
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
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Best Local S
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LENGTH: 943
                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Paenibacillus macerans -09-969-362-5
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: OP1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Ton
APPLICANT: AOYAGI, MOTI
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TITLE OF INVENTION: A 2,6,-b-D-Fructan Hydrolase Enzyme And
TITLE OF INVENTION: Process For Using The Enzyme
FILE REFERENCE: 5540.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                      1204 YRQSGYGTDGV 1214
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Local Similarity 50.0%;
nes 6; Conservative
                                                                                                                              3 YRASALGSDGV 13
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                                                                                                                                                                      Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HASEGAWA, Makoto
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                                                                                                                                                                        Conservative
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                                                                                                                                                                                            47.4%;
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                                                                                                                                                                   Score 37; DB y; Lc
Pred. No. 1.6e+02;
""" matches 3;
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Query Match
Best Local Similarity
7; Conserva
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APPLICANT:
APPLICANT:
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APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriichi
                                                                                                                                                                                                   SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: Insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
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Matches 7; Conserv
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APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeţide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: poynucleotide encoding the same
FILE REFERENCE: 0P1335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR APPLICATION NUMBER: JP 2001-203463
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-203463
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                                                                                                                                                          LENGTH: 1386
TYPE: PRT
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                                                                                                                                         ORGANISM: Bacillus popilliae
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3 YRASALGSDGV 13
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                                           Conservative
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63.6%;
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Pred. No. 1.6e+02;
Pred. No. 3;
                                                           Pred. No. 1.7e+02;
                                                                              Score 37;
                                           Mismatches
                                                                                DB 9;
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1238 YRQSGYGTDGV 1248

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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-40694
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 40694
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                     OTHER INFORMATION: MAP TO AL133458.11
OTHER INFORMATION: EXPRESSED IN PLACESTA, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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FILING DATE: 2001-01-30
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                                                                                                                            EXPRESSED
EXPRESSED
                                                                                                 EST_HUMAN HIT: BF329911.1, EVALUE 4.00e-15
  46.28;
57.18;
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                                                                                                                          IN BONE MARROW, SIGNAL = 4.5
IN LUNG, SIGNAL = 5.1
IN FETAL LIVER, SIGNAL = 4.3
Score 36;
Pred. No.
DB 10;
5.3;
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                     Length 50
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
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US-09-738-626-4829
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US-09-815-242-11279
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; SOFTWARE: FastSEQ f
; SEQ ID NO 11279
; LENGTH: 295
                                                                                                                                                                                                          Sequence 4829, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 7; Conserv
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                          APPLICANT:
                                                                                                                                     APPLICANT:
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                                                                    ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                            MIZOGUCHI,
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Trawick, John D.
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Zyskind, Judith W.
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                                                      IKEDA, MASATO
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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ESEQ for Windows Version 4.0
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Pred. No.
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د.
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PRIOR PRIOR APPLICATION NUMBER: 60/059352

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PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 4829
LENGTH: 358
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APPLICANT:
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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                                                                                                                                                                                                  APPLICATION NUMBER: 60/059122
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Godowski, Paul J.
Gurney, Austin L.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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PRIOR APPLICATION NUMBER: 00/063704
PRIOR ETLING DATE: 1997-10-29
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PRIOR APPLICATION NUMBER: 60/063733
PRIOR APPLICATION NUMBER: 60/063733
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12 PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/063755 FILING DATE: 1997-10-17 APPLICATION NUMBER: FILING DATE: 1997-10 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/063082 FILING DATE: 1998-02-09
APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/066511 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/066364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/064248 APPLICATION NUMBER: 60/063738 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063045 APPLICATION NUMBER: 60/062285 APPLICATION NUMBER: 60/072320 FILING DATE: 1998-01-23 APPLICATION NUMBER: 60/073612 FILING DATE: 1998-02-04 APPLICATION NUMBER: 60/069334 APPLICATION NUMBER: 60/069278 APPLICATION NUMBER: 60/066770 APPLICATION NUMBER: 60/066453 APPLICATION NUMBER: 60/065846 APPLICATION NUMBER: FILING DATE: 1997-1: FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/074092 APPLICATION NUMBER: 60/074086 APPLICATION NUMBER: 60/069212 1997-10-1997-10-24 1997-10-24 1997-10-1997-10-24 1997-10-31 1997-10-29 1997-10-29 1997-10-24 1997-11-24 1997-11-17 1997-10-28 1997-12-11 1997-11-24 1997-12-16 60/062814 60/062287 60/063550 60/063329 60/063327 60/063127 60/062816 60/069694

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PRIOR
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DR FILING DATE: 1998-06-10
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/08026
OR FILING DATE: 1998-06-04
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088741
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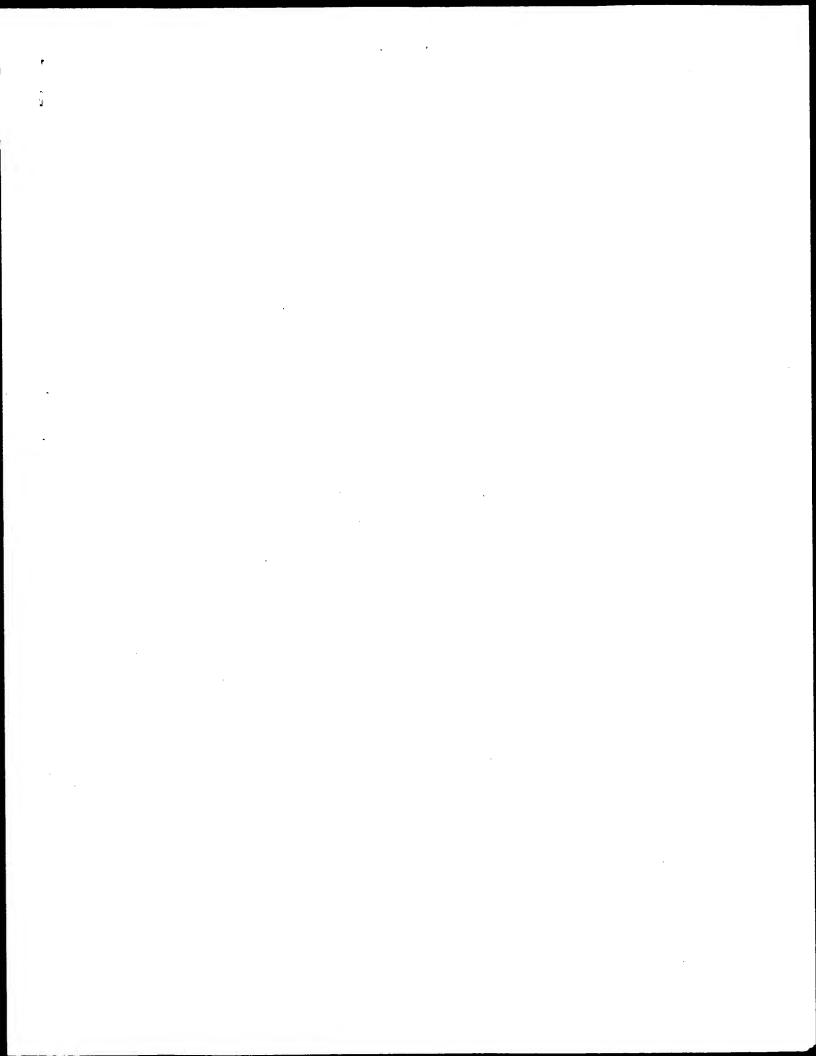
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081695
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FILING DATE: 1998-05-13
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/081818
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APPLICATION NUMBER: 60/081817
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Search completed: January 16, 2003, 10:16:53 Job time: 12 secs



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Result
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38.5
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78
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                                                                                                                                                       hypothetical prote
protein C38C10.5a
protein C38C10.5b
protein F6N18.2 [i
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hypothetical prote
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#text_change 03-Jun-2002	C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C:Accession: S48029; A47881; C64877	vision 1877	, C64	equence 47681;	1999 #s 8029; A	10-Sep-	C; Date: 10-Sep-1999 #sequence_revis C; Accession: S48029; A47681; C64877 B: Kater M M : Koringston M 4877
reductase; short-chain alcohol dehydrogenase homolog	short-chain alc	luctase;	rec	yl-ACP coli	es: eno erichia	ate nam	N;Alternate names: enoyl-ACP C;Species: Escherichia coli
	(NADH2) (EC 1.3.1.9)	reductase	rec	otein]	rier-pr	cyl-car	enoyl-[acyl-carrier-protein]
						·	RESULT 1 S48029
	ALIGNMENTS	ALI					
probable sugar tra	_	C84593	N	547	48.7	38	45
indole-3-pyruvate		S44486	_	545		38	44
hypothetical prote		F70776	2	513	48.7	38	43
probable periplasm		G97499	ν	492	œ	38	42
cyaE protein - Bor		BVBRCE	μ.	474	œ	38	41
conserved hypothet	_	AC2718	ν	452	48.7	38	40
hasA export system	_	в49933	N	437	∞	38	39
glutamate-1-semial	_	E81358	N	424	48.7	38	38
probable flagellar		D71297	N	416	48.7	38	37
probable hexosyltr	,	A70571		378	œ	38	36
probable glycosylt		D86965	N	374	48.7	38	35
HPr(ser-P)kinase/p		E98030	N	316	48.7	38	34
Hpr(Ser) kinase/ph		F95164	ν	312	48.7	38	33
enoyl-(acyl-carrie		AG2669	N	272	48.7	38	32
hypothetical prote		E97451	N	272	48.7	38	31
adenylylsulfate 3-		н69285	N	155	48.7	38	30

A; Residues: 1-262 <BLAT>
A; Residues: 1-262 <BLAT>
A; Residues: 1-262 <BLAT>
A; Cross-references: GB:AE000227; GB:U00096; NID:g1787543; PIDN:AAC74370.1; PID:g17875
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: fab1; envM
C; Function:
A; Gene: fab1; envM
A; Gene: fab1; envM
A; Gene: fab1; envM
A; Gene: fab2; envM
A; Gene: fab3; envM
A; Gene: fab4; envM
A; Gene: fab4; envM
A; Osciption: catalyzes reduction by NADH of enoy1-acy1-carrier-protein to the corre
A; Pathway: fatty acid biosynthesis
A; Note: inhibited by palmitoy1-CoA and diazaborine
C; Superfamily: enoy1-lacy1-carrier-protein] reductase (NADH); short-chain alcohol deh
C; Keywords: fatty acid biosynthesis; homotetramer; inner membrane; NAD; oxidoreductas
F; 7-190/Domain: short-chain alcohol dehydrogenase homology <SADH>
F; 9-35/Region: NAD binding J. Gen. Microbiol. 138, 2093-2100, 1992
A;Title: Sequences of the envM gene and of two mutated alleles in Escherichia coli.
A;Reference number: A47681; MUID:93123967; PMID:1364817
A;Accession: A47681 Query Match
Best Local Similurity
"hehes 9; Conserva A;Molecule type: DNA
A:Residues: 1-262 cdBFx,
A:Residues: 1-262 cdBFx,
A:Cross-references: GB:M97219; NID:g145850; PIDN:AAA17755.1; PID:g145851
A:Cross-references: GB:M97219; NID:g145850; PIDN:AAA17755.1; PID:g145851
A;Note: sequence extracted from NCBI backbone (NCBIN:121825, NCBIP:121826)
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997 A:Molecule type: DNA
A:Residues: 1-262 <KAT>
A:Residues: 1-262 <KAT>
A:Cross-references: EMBL:X78733; NID:g587105; PIDN:CAA55381.1;
A:Experimental source: strain K-12, substrain W3110
R:Bergler, H.: Hogenauer, G.; Turnowsky, F.
J. Gen. Microbiol. 138, 2093-2100, 1992
J. Gen. Microbiol. 138, 2093-2100, 1992 A;Title: The complete genome sequence of Escherichia coll K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: C64877 R;Rater, M.M.; KONINGSTEIN, G.M.; NIJKAMP, H.J.J.; Stultje, A.R.
Plant Mol. Biol. 25, 771-790, 1194
A;Title: The use of a hybrid genetic system to study the functional relationship betw A;Reference number: \$48029; MUID:94355651; PMID:8075395
A;Accession: \$48029 A; Molecule type: DNA A; Status: nucleic acid sequence not shown; A; Status: preliminary A; Status: preliminary 62.8%; Score 49; DB Pred. No. 0.44 4; Mismatches translation not shown DB 1; 0.44; Length 262 PID:9587106 Riley, M.; trai

Conservative

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Indels

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Gaps

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A; Note: inhibited by diazabo
C; Superfamily: enoy1-[acy1-c
C; Keywords: fatty acid blosy
F;7-190/Domain: short-chain
F;9-35/Region: NAD binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M31806; NID:g153953; PIDN:AAA27059.1; PID:g153955 R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D. Mol. Microbiol. 17, 523-531, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: envM genes of Salmonella typhimurium and Escherichia A;Reference number: A43729; MUID:90078098; PMID:2687243 A;Accession: B43729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: B43729; S70724
R; Turnowsky, F.; Fuchs, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enoy1-[acy1-carrier-protein] reductase (NADH2) (EC 1.3.1.9) - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 10-Sep_199  #sequence_revision 10-Sep-1999  #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
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                                                                                                                                                                                                                                              gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shi
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: E90861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophi A;Reference number: S70719; MUID:96100451; PMID:8559071 A;Accession: S70724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-262 <TI
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A; Residues: 'X', 3-4, 'X', 6-11 <QIS>
                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-262 <HAY>
A;Residues: 1-262 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35284.1; PID:g13361326; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                            enoy1-[acy1-carrier-protein] reductase (NADH) ECs1861 [imported] - Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain SL1344
                                                                                                        A; Gene: ECs186:
C; Superfamily:
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             Matches
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                                                            Query Match
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Bacteriol. 171, 6555-6565, 1989
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les 9; Conserv
                                             Local
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T.; Makino, K.; Ohnishi, M.;
Vacunada. T.; Kuhara, S.;
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د يو)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fatty acid biosynthesis;
                                             Similarity
                                                                                                          enoyl-[acyl-carrier-protein] reductase (NADH); short-chain
                          Conservative
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60.0%;
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                                             62.8%;
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                            4;
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Pred. No. 0.44;
                                             Score 49; DB 2
Pred. No. 0.44;
                              Mismatches
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Shiba, T.; Hattori, M.;
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                                  C; Species: Proteus r
C; Date: 19-Mar-1997
                                                    enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) - C;Species: Proteus mirabilis
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A; Title: Genome sequence of A; Reference number: A85480; A; Accession: H85757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_challonger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: fab!
C;Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005174; NID:g12515500; PIDN:AAG56524.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-262 <STO>
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                                                                                                                                                                                                                                                                                                                                                             A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant A; Reference number: ABO502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Parkhill, J.; Dougan, G.; James, N.D., A., R;Parkhill, J.; Cronin, A.; Davis, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enoyl-[acyl-carrier-protein] reductase (NADH) STY1352 [imported] -
                                                                                                                                                                           C; Superfamily: enoyl-{acyl-carrier-protein} reductase (NADH); short-chain alcohol
                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-262 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                , s.; Moule, s.; O'Gaora, P. Nature 413, 848-852, 2001
                                                                                                                                                                                                     A; Gene: STY1352
                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                      A; Accession: AD0656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: AD0656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                        Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRYRASALGSDGVRV 15
                                          1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRYMANAMGPEGVRV 184
VRYMANAMGPEGVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                     GB:AL513382;
                                                                                                               62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.8%;
  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterohemorrhagic Escherichia coli 0157:H7
MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                     PIDN:CAD01621.1; PID:g16502475; GSPDB:GN00176
                                                                                            4
                                                                                                               Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 2
Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomson, N.R.; Pickard, D.; Wain, J.; P.; Davies, R.M.; Dowd, L.; White, N
                                                                                                                    0.44;
                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                       Length 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                               Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                    Skelton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPDB:GN00145;
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                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 enterica
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                                                                                                                                                                                                                                                                                                                                                                                                                    Stevens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.; Farr
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#sequence_revision

25-Apr-1997

#text_change 03-Jun-2002

Proteus mirabilis

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2354
                                                                                                                                                                                                                                                     C; Species: Nostoc sp. atrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AC2354
A;Cross-references: GB:BA000019; PIDN:BAB76090.1; PID:g17133527; GSPDB:GN00179
                                       A; Molecule type: DNA
A; Residues: 1-264 < KUR>
                                                                                                                                                                                                                                                                                                                                                                      enoyl-[acyl-carrier-protein] reductase [imported] - Nostoc sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: fabI; BU265
C;Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydr
C;Keywords: oxidoreductase
                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-260 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Shigenobu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002 C;Accession: G84960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) [imported] - Buchnera sp.
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C;Superfamily: enoyl-lacyl-carrier-protein) reductase (NADH); short-chain alcohol dehydr
C;Keywords: fatty acid biosynthesis; inner membrane; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Accession: S71883

R:Perilto, B.; Allocati, N.; Casalone, E.; Masulli, M.; Dragani, B.; Polsinelli, M.; Acet Blochem. J. 318, 157-162, 1996

A;Title: Molecular cloning and overexpression of a glutathione transferase gene from Pro A;Reference number: S71882; MUID:96358500; PMID:8761466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: preliminary
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A;Experimental source: strain AF 2924
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A; Residues: 1-99 < PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 VRYMASSLGKENIRV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRYRASALGSDGVRV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VRYMANAMGPEGIRV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-99 <PER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.78;
53.38;
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53.3%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 260; 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                      RESULT 11
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A:Introns: 412/1; 612/2; 670/3; 676/3; 729/3; 914/2; 984/1
C:Superfamily: Caenorhabditis elegans hypothetical protein C38C10.5
                                                                                                                                                                                                                                                           A; Molecule type: DNA
A: Residues: 1-1112 <THO>
                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 21-Jan-2000
C:Accession: S28289
                                                                                                                                                                                                                                         A; Cross-references: EMBL: Z19153
                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: $28289
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C38ClO.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, : Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                             R;Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S28289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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A; Residues: 1-265 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: C83419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Gene: all4391
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol deh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH-dependent enoyl-ACP reductase PA1806 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
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                                                                                         Matches 8; Conserv
                                                                                                                                Query Match
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1040 IRFRASQMNGDGVNAT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 VRYLAGSLGAEGTRV 187
                                           1 MRYRASALGSDGVRVT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                      Conservative
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                                                                                                      56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.4%;
53.3%;
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                                                                                                      Score 44;
Pred. No.
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Pred. No. 3.5;
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                                                                                    Mismatches
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                                                                                5.
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                                                                                Indels
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                                                                           Gaps
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                                                                                0
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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A; February and A; F
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C;Accession: A88554
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A;Residues: 1-1385 <STO>
A;Cross-references: GB:Chr_III; PIDN:CAA79551.1; PID:g3874875; GSPDB:GN00021; CESP:C38C1
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Aug-2002
C;Accession: B88554
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        ansen, N.F.; Hughes, B.; Huizar, I
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins,
C.A.; Li, J.H.; Li. v . r;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: C38C10.5b
A;Map position: 3
C;Superfamily: Caenorhabditis elegans hypothetical protein C38C10.5
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A;Note: published_errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                   protein F6N18.2 (imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A;Residues: 1-1391 <STO>
A;Residues: 1-1391 <STO>
A;Cross-references: GB:Chr_III; PIDN:CAA82365.1; PID:g3880296; GSPDB:GN00021; CESP:C38C1
A;Cross-references: GB:Chr_III; PIDN:CAA82365.1; PID:g3880296; GSPDB:GN00021; CESP:C38C1
A;Note: CDNA EST EMBL:C11839 comes from this gene
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                                                                                                                                                                    R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
                                                                                                                                                                                                                                                  C; Accession: F86451
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Li, J.H.; Li, Y.; Lin, X.; Liu,
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nes 8; Conserv
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8; Conserv
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50.0%;
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                        Johnson-Hopson, C.; Khan, S.X.; Liu, Z.A.; Luros, J
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                                    n, S.; Khaykin, E
J.S.; Maiti, R.;
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                                                                                                                                                                                                                                     probable serine/threonine-specific protein kinase (EC 2.7.1.-) F8D20.110 - Arabidopsi
N;Alternate names: protein F8D20.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                     A; Reference number: Z15381
                                                                                  submitted to the Protein Sequence Database, July 1998
                                                                                                                           R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse,
                                                                                                                                                                                                     C;Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
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T04665

T.; Heijnen, L.; Vos,

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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86451
A;Status: preliminary
A;Status: preliminary
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R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: D95284
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A; Residues: 1-291 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95284
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                                                                                                                                                                                                                                                                                     A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; I hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE006469; PIDN:AAK64838.1; PID:g14523251; GSPDB:GN00165
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A; Residues: 1-258 < KUR>
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                                                                                                                                                         A;Genome: plasmid
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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Matches 8; Conserv
                                                    Matches
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5 ASALGSDGVRV 15
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72.7%;
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Pred. No.
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